

SEQUENCE LISTING

<110> Thompson, John E.
 Wang, Tzann-Wei
 Lu, Dongen Lilly

<120> DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
 PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
 DEATH IN PLANTS

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<150> 09/348,675
 <151> 1999-07-06

<160> 35

<170> PatentIn Ver. 2.1

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 Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
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ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc 152
 Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
 20 25 30

tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg 200
 Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
 35 40 45

gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att 248
 Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
 50 55 60 65

gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag 296
 Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
 70 75 80

gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc 344
 Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
 85 90 95

tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt 392
 Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val

DC01 345180 v 1

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Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala			
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cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg			536
Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser			
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Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr			
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Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu			
180	185	190	
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Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala			
195	200	205	
cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct			728
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Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser			
230	235	240	
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Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp			
245	250	255	
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Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile			
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275	280	285	
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Met Ile Ile Leu Gly Gly Leu Pro Lys His His Val Cys Asn Ala			
290	295	300	305
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Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val			
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340	345	350	
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Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala			
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Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala 50 55 60
Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr 65 70 75 80
Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val 85 90 95
Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly 100 105 110
Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val 115 120 125
Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu 130 135 140
Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg 145 150 155 160
Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn 165 170 175
Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr 180 185 190
Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile 195 200 205

Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
210 215 220

Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
225 230 235 240

Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
245 250 255

Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
260 265 270

Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
275 280 285

Gly Met Ile Ile Leu Gly Gly Leu Pro Lys His His Val Cys Asn
290 295 300

Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
305 310 315 320

Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
325 330 335

Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
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<220>
<223> Description of Artificial Sequence: primer

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1154..1258, 1575..1862)

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ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga		157
Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly		
15 20 25 30		
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Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met		
35 40 45		
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Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val		
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gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaaa attccttctt		305
Val Asn Gln Met		
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Phe Glu Phe Val		
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Cys Ser Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys		
90 95 100		
aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga		503
Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg		
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gat act att cgt tat ctt gtt cag cat cat atg gtttgatt tttgtttat		556
Asp Thr Ile Arg Tyr Leu Val Gln His His Met		
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tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat		665
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Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile		
180 185 190		
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Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu		
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35 40 45	
Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val Val Asn	
50 55 60	
Gln Met Phe Glu Phe Val Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu	
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Thr Thr Val Ala Glu Asp Cys Ser Glu Glu Lys Asn Pro Ser Phe	
85 90 95	
Arg Glu Ser Val Lys Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu	
100 105 110	
Val Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His	
115 120 125	
Met Val Asp Val Ile Val Thr Thr Gly Gly Val Glu Glu Asp Leu	
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145 150 155 160	
Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val	
165 170 175	
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Phe	
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195 200 205	
Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu Ile Asn Asn Glu Ser Ser	
210 215 220	
Tyr Leu Tyr Trp Ala Tyr Lys Met Asn Ile Pro Val Phe Cys Pro Gly	
225 230 235 240	
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg	
245 250 255	
Thr Ser Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala Met Asn	
260 265 270	
Gly Glu Ala Val His Ala Asn Pro Lys Lys Thr Gly Met Ile Ile Leu	
275 280 285	

Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg
290 295 300

Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln Glu Phe Asp
305 310 315 320

Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: primer

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<213> Dianthus sp.

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<222> (256)..(1374)

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attgaactac tgcaattcta aaactttgtt tacatttaa ttccatcaaa gattgagttc 240

agcatagggaa aaagg atg gag gat gct aat cat gat agt gtg gca tct gcg 291

Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala

1

5

10

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His Ser Ala Ala Phe Lys Ser Glu Asn Leu Glu Gly Lys Ser Val

DRAFT

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gcc att gaa gta gtt aat cat atg cta gat tgg agt ctg gca gat gag Ala Ile Glu Val Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu 65 70 75			483
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att cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc Ile Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile 190 195 200			867
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Ser Trp Gly Lys Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys	
335 340 345	
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Lys Arg Glu Lys Glu Arg Lys Ser Cys	
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35 40 45	
Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Glu Val	
50 55 60	
Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu Ala Pro Val Asp	
65 70 75 80	
Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg Glu Ser Val Lys	
85 90 95	
Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile Ser Ser Gly Val	
100 105 110	
Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met Val Asp Val Ile	

DC01 345180 v1

115	120	125
Val Thr Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile Lys Gly Arg Ser		
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145	150	155
160		
Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val		
165	170	175
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Leu		
180	185	190
Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp Thr Pro		
195	200	205
Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu Ser Ser		
210	215	220
Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys Pro Gly		
225	230	235
240		
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg		
245	250	255
Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile Arg Ala Val Asn		
260	265	270
Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile Ile Leu		
275	280	285
Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg		
290	295	300
Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala Glu Glu Phe Asp		
305	310	315
320		
Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile Ser Trp Gly Lys		
325	330	335
Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile		
340	345	350
Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala Lys Arg Glu Lys		
355	360	365
Glu Arg Lys Ser Cys		
370		
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<211> 780		
<212> DNA		
<213> Lycopersicon sp.		
<220>		
<223> eif-5A		
<220>		
<221> CDS		
<222> (43)..(522)		
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aaagaatcct agagagagaa agggaatcct agagagagaa gc atg tcg gac gaa		54
Met Ser Asp Glu		

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1

gaa cac cat ttt gag tca aag gca gat gct ggt gcc tca aaa act ttc	102
Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala Ser Lys Thr Phe	
5 10 15 20	
cca cag caa gct gga acc atc cgt aag aat ggt tac atc gtt atc aaa	150
Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val Ile Lys	
25 30 35	
ggc cgt ccc tgc aag gtt gtt gag gtc tcc act tca aaa act gga aaa	198
Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys	
40 45 50	
cac gga cat gct aaa tgt cac ttt gtg gca att gac att ttc aat gga	246
His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly	
55 60 65	
aag aaa ctg gaa gat atc gtt ccg tcc tcc cac aat tgt gat gtg cca	294
Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp Val Pro	
70 75 80	
cat gtt aac cgt acc gac tat cag ctg att gat atc tct gaa gat ggt	342
His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly	
85 90 95 100	
ttt gtc tca ctt ctt act gaa agt gga aac acc aag gat gac ctc agg	390
Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys Asp Asp Leu Arg	
105 110 115	
ctt ccc acc gat gaa aat ctg ctg aag cag gtt aaa gat ggg ttc cag	438
Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys Asp Gly Phe Gln	
120 125 130	
gaa gga aag gat ctt gtg gtg tct gtt atg tct gcg atg ggc gaa gag	486
Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly Glu Glu	
135 140 145	
cag att aac gcc gtt aag gat gtt ggt acc aag aat tagttatgtc	532
Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn	
150 155 160	
atggcagcat aatcaactgcc aaagcttaa gacattatca tatcctaattg tggtactttg	592
atatacactag attataaact gtgttatgg cactgttcaa aacaaaagaa agaaaactgc	652
tgttatggct agagaaaagta ttggcttga gctttgaca gcacagttga actatgtgaa	712
aattctactt tttttttttt gggtaaaaata ctgctcggtt aatgtttgc aaaaaaaaaa	772
aaaaaaa	780

<210> 12
 <211> 160
 <212> PRT
 <213> Lycopersicon sp.

<220>
 <223> eif-5A

<400> 12
 Met Ser Asp Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala
 1 5 10 15
 Ser Lys Thr Phe Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr

20	25	30	
Ile Val Ile Lys Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser			
35	40	45	
Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp			
50	55	60	
Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn			
65	70	75	80
Cys Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile			
85	90	95	
Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys			
100	105	110	
Asp Asp Leu Arg Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys			
115	120	125	
Asp Gly Phe Gln Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala			
130	135	140	
Met Gly Glu Glu Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn			
145	150	155	160
<210> 13			
<211> 812			
<212> DNA			
<213> Dianthus sp.			
<220>			
<223> eif-5A			
<220>			
<221> CDS			
<222> (67)..(546)			
<400> 13			
ctctttaca tcaatcgaaa aaaaattagg gttcttattt tagagtgaga ggcgaaaaat	60		
cgaacg atg tcg gac gac gat cac cat ttc gag tca tcg gcc gac gcc		108	
Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala	1	5	10
gga gca tcc aag act tac cct caa caa gct ggt aca atc cgc aag agc		156	
Gly Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser	15	20	25
			30
ggt cac atc gtc atc aaa aat cgc cct tgc aag gtg gtt gag gtt tct		204	
Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser	35	40	45
acc tcc aag act ggc aag cac ggt cat gcc aaa tgt cac ttt gtt gcc		252	
Thr Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala	50	55	60
att gac att ttc aac ggc aag aag ctg gaa gat att gtc ccc tca tcc		300	
Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser	65	70	75
cac aat tgt gat gtt cca cat gtc aac cgt gtc gac tac cag ctg ctt		348	
His Asn Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu	80	85	90

gat atc act gaa gat ggc ttt gtt agt ctg ctg act gac agt ggt gac 396
 Asp Ile Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp
 95 100 105 110

 acc aag gat gat ctg aag ctt cct gct gat gag gcc ctt gtg aag cag 444
 Thr Lys Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln
 115 120 125

 atg aag gag gga ttt gag gcg ggg aaa gac ttg att ctg tca gtc atg 492
 Met Lys Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met
 130 135 140

 tgt gca atg gga gaa gag cag atc tgc gcc gtc aag gac gtt agt ggt 540
 Cys Ala Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly
 145 150 155

 ggc aag tagaagcttt tcatgtatcc aatactacgc ggtgcagttg aagcaatagt 596
 Gly Lys
 160

 aatctcgaga acattctgaa ccttatatgt tgaattgatg gtgccttagtt tgttttggaa 656
 atctcttgc aattaagttg tacccaaatca atggatgtaa tgtcttgaat ttgttttatt 716
 tttgtttga tggttgctgt gattgcatta tgcattgtta tgagttatga cctgttataa 776
 cacaaggaaa tggtaaaaaa aaaaaaaaaa aaaaaaa 812

 <210> 14
 <211> 160
 <212> PRT
 <213> Dianthus sp.

 <220>
 <223> eif-5A

 <400> 14
 Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala Gly Ala
 1 5 10 15

 Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser Gly His
 20 25 30

 Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
 35 40 45

 Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
 50 55 60

 Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
 65 70 75 80

 Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu Asp Ile
 85 90 95

 Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp Thr Lys
 100 105 110

 Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln Met Lys
 115 120 125

 Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met Cys Ala
 130 135 140

 Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly Gly Lys

145	150	155	160
<210> 15 <211> 702 <212> DNA <213> Arabidopsis sp.			
<220> <223> eif-5A			
<220> <221> CDS <222> (56)...(529)			
<400> 15 ctgttaccaa aaaatctgta ccgcaaaatc ctcgtcgaag ctcgctgctg caacc atg 58 Met 1			
tcc gac gag gag cat cac ttt gag tcc agt gac gcc gga gcg tcc aaa 106 Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser Lys 5 10 15			
acc tac cct caa caa gct gga acc atc cgt aag aat ggt tac atc gtc 154 Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val 20 25 30			
atc aaa aat cgt ccc tgc aag gtt gtt gag gtt tca acc tcg aag act 202 Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr 35 40 45			
ggc aag cat ggt cat gct aaa tgt cat ttt gta gct att gat atc ttc 250 Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe 50 55 60 65			
acc agc aag aaa ctc gaa gat att gtt cct tct tcc cac aat tgt gat 298 Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp 70 75 80			
gtt cct cat gtc aac cgt act gat tat cag ctg att gac att tct gaa 346 Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu 85 90 95			
gat gga tat gtc agt ttg ttg act gat aac ggt agt acc aag gat gac 394 Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp Asp 100 105 110			
ctt aag ctc cct aat gat gac act ctg ctc caa cag atc aag agt ggg 442 Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser Gly 115 120 125			
ttt gat gat gga aaa gat cta gtg gtg agt gta atg tca gct atg gga 490 Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly 130 135 140 145			
gag gaa cag atc aat gct ctt aag gac atc ggt ccc aag tgagactaac 539 Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys 150 155			
aaagcctccc ctttgttatg agattcttct tcttcgttag gcttccatata ctcgtcggag 599			
attatcttgt ttttgggtta ctcctatttt ggatattaa actttgtta ataatgccat 659			
cttcttcaac cttttccttc tagatggttt ttatacttct tct 702			

<210> 16
<211> 158
<212> PRT
<213> Arabidopsis sp.

<220>
<223> eif-5A

<400> 16
Met Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser
1 5 10 15
Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile
20 25 30
Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys
35 40 45
Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile
50 55 60
Phe Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys
65 70 75 80
Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser
85 90 95
Glu Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp
100 105 110
Asp Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser
115 120 125
Gly Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met
130 135 140
Gly Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
145 150 155

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
aaarrycgmcytgcaaggt 20

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
aatacgaactc actatacg 17

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<223> "n" bases represent a, t, c, g, other or unknown

<400> 19
tcytnccyt cmkctaaahcc 20

<210> 20
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
attaaccctc actaaag 17

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
ctgttaccaa aaaatctgta cc 22

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
agaagaagta taaaaaccat c 21

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
aaagaatcct agagagagaa agg 23

<210> 24
<211> 18
<212> DNA

caa gat atc aga gct atg aac ggc gaa gct gtc cat gca aat cct aaa	432
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys	
130 135 140	
aag aca ggg atg ata atc ctt gga ggg ggc ttg cca aag cac cac ata	480
Lys Thr Gly Met Ile Ile Leu Gly Gly Leu Pro Lys His His Ile	
145 150 155 160	
tgt aat gcc aat atg atg cgc aat ggt gca gat tac gct gta ttt ata	528
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile	
165 170 175	
aac acc ggg caa gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat	576
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp	
180 185 190	
gaa gc	581
Glu	
<210> 27	
<211> 522	
<212> DNA	
<213> Dianthus sp.	
<220>	
<223> DHS	
<220>	
<221> CDS	
<222> (3)...(521)	
<400> 27	
ga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt gcc	47
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala	
1 5 10 15	
tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt aat	95
Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn	
20 25 30	
ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc att	143
Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile	
35 40 45	
cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc tta	191
Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu	
50 55 60	
tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac gat	239
Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp	
65 70 75	
gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta ttt	287
Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe	
80 85 90 95	
tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt cat	335
Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His	
100 105 110	
tct ttt cgc aat ccg ggt tta atc atc gat gtt gtg caa gat ata aga	383
Ser Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg	
115 120 125	
gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc atg	431

Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met
 130 135 140
 att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca aac 479
 Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn
 145 150 155
 atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac acc g 522
 Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
 160 165 170

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 28 24
 ttgargaaaga tycatmaart gcct

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 29 23
 ccatcaaayt cytgkgrgt gtt

<210> 30
 <211> 484
 <212> DNA
 <213> Arabidopsis sp.

<220>
 <223> DHS

<220>
 <221> CDS
 <222> (2)..(112)

<400> 30 49
 t gca cgc cct gat gaa gct gtg tct tgg ggt aaa att agg ggt tct gct
 Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
 1 5 10 15

aaa acc gtt aag gtc tgc ttt tta att tct tca cat cct aat tta tat 97
 Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
 20 25 30

ctc act cag tgg ttt tgagtacata tttaatattt gatcattttt gcaggataac 152
 Leu Thr Gln Trp Phe
 35

tgtgatgcta ccatagcattt cccattgtt gttgcagaaa catttgccac aaagagagac 212
 caaacctgtg agtctaagac ttaagaactg actggcggtt ttggccatgg attcttaaag 272
 atcggttgcatttttta cactggagtg accatataac actccacattt gatgtggctg 332

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tgacgcgaat tgtcttcttg cgaattgtac ttttagttct ctcaacctaa aatgattgc 392
agattgtgtt ttcgtttaaa acacaagagt cttgttagtca ataatcctt gccttataaa 452
attattcagt tccaaacaaaa aaaaaaaaaa aa 484

<210> 31
<211> 559
<212> DNA
<213> Lycopersicon sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (1)..(156)

<220>
<223> "n" bases represent a, t, c, g, other or unknown

<400> 31 48
ggt gct cgt cct gat gaa gct gta tca tgg gga aag ata cgt ggt ggt
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
1 5 10 15

gcc aag act gtg aag gtg cat tgt gat gca acc att gca ttt ccc ata 96
Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
20 25 30

tta gta gct gag aca ttt gca gct aag agt aag gaa ttc tcc cag ata 144
Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
35 40 45

agg tgc caa gtt tgaacattga ggaagctgtc cttccgacca cacatatgaa 196
Arg Cys Gln Val
50

ttgctagctt ttgaagccaa ctgtcttagtg tgcatcacca tttattctgc aaaactgact 256
agagagcagg gtatattcct ctaccccgag ttagacgaca tcctgtatgg ttcaattaa 316
ttatatttct ccccttcaca coatgttatt tagttcttt cctttcgaa agtgaagagc 376
tttagatgttc ataggtttg aattatgttg gaggttgggt ataactgact agtccttta 436
ccatatagat aatgtatcct tgcactatga gatttgggt gtgtttgata ccaaggaaaa 496
atgtttatggggaaacaat tggatttta attaaaaaaaaa aattgnttaa aaaaaaaaaa 556
aaa 559

<210> 32
<211> 193
<212> PRT
<213> Arabidopsis sp.

<220>
<223> DHS

<400> 32
Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
1 5 10 15

Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
20 25 30

Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
35 40 45

Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
50 55 60

Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
65 70 75 80

Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
85 90 95

Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
100 105 110

Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
115 120 125

Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys
130 135 140

Lys Thr Gly Met Ile Ile Leu Gly Gly Leu Pro Lys His His Ile
145 150 155 160

Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile
165 170 175

Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp
180 185 190

Glu

<210> 33
<211> 173
<212> PRT
<213> Dianthus sp.

<220>
<223> DHS

<400> 33
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu
1 5 10 15

Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu
20 25 30

Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro
35 40 45

Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp
50 55 60

Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu
65 70 75 80

Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys
85 90 95

Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser
100 105 110

Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala
115 120 125
Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile
130 135 140
Ile Leu Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met
145 150 155 160
Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
165 170

<210> 34
<211> 37
<212> PRT
<213> *Arabidopsis* sp.

<220>
<223> DHS

<400> 34
Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
1 5 10 15
Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
20 25 30
Leu Thr Gln Trp Phe
35

<210> 35
<211> 52
<212> PRT
<213> *Lycopersicon* sp.

<220>
<223> DHS
<400> 35
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
1 5 10 15
Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
20 25 30
Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
35 40 45
Arg Cys Gln Val
50